OSTO
1009

#2

OIPE

RAW SEQUENCE LISTING   DATE: 01/03/2002
PATENT APPLICATION: US/09/944,884   TIME: 11:21:13

Input Set : N:\Crf3\RULE60\09944884.raw
Output Set: N:\CRF3\01032002\I944884.raw

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 1 <110> APPLICANT: Baker, Kevin
 2         Botstein,David
 3         Eaton,Dan
 4         Ferrara,Napoleone
 5         Filvaroff,Ellen
 6         Gerritsen,Mary
 7         Goddard,Audrey                    ENTERED
 8         Godowski,Paul
 9         Grimaldi,Christopher
10         Gurney,Austin
11         Hillan,Kenneth
12         Kljavin,Ivar
13         Napier,Mary
14         Roy,Margaret
15         Tumas,Daniel
16         Wood,William
17 <120> TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
18         ACIDS ENCODING THE SAME
19 <130> FILE REFERENCE: P2548P1C1
20 <140> CURRENT APPLICATION NUMBER: 09/944,884
21 <141> CURRENT FILING DATE: 2001-08-31
22 <150> PRIOR APPLICATION NUMBER: 09/866,028
23 <151> PRIOR FILING DATE: 2001-05-25
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28 <211> LENGTH: 2454
29 <212> TYPE: DNA
30 <213> ORGANISM: Homo Sapien
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33         caccaggact gtgttgaagg gtgtttttttt tcttttaaat gtaatacctc 100
34         ctcatctttt cttcttacac agtgtctgag aacatttaca ttatagataa 150
35         gtagtacatg gtggataact tctactttta ggaggactac tctcttctga 200
36         cagtcctaga ctggtcttct acactaagac accatgaagg agtatgtgct 250
37         cctattattc ctggctttgt gctctgccaa acccttcttt agcccttcac 300
38         acatcgcact gaagaatatg atgctgaagg atatggaaga cacagatgat 350
39         gatgatgatg atgatgatga tgatgatgat gatgaggaca actctctttt 400
40         tccaacaaga gagccaagaa gccatttttt tccatttgat ctgtttccaa 450
41         tgtgtccatt tggatgtcag tgctattcac gagttgtaca ttgctcagat 500
42         ttaggtttga cctcagtccc aaccaacatt ccatttgata ctcgaatgct 550
43         tgatcttcaa aacaataaaa ttaaggaaat caaagaaaat gattttaaag 600
44         gactcacttc actttatggt ctgatcctga acaacaacaa gctaacgaag 650
45         attcacccaa aagcctttct aaccacaaag aagttgcgaa ggctgtatct 700
46         gtcccacaat caactaagtg aaataccact taatcttccc aaatcattag 750
47         cagaactcag aattcatgaa aataaagtta agaaaataca aaaggacaca 800
48         ttcaaaggaa tgaatgcttt acacgttttg gaaatgagtg caaaccctct 850
49         tgataataat gggatagagc caggggcatt tgaagggggtg acggtgttcc 900
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51        ccaactttat tggagcttca cttagattat aataaaattt caacagtgga 1000
52        acttgaggat tttaaacgat acaaagaact acaaaggctg ggcctaggaa 1050
53        acaacaaaat cacagatatc gaaaatggga gtcttgctaa cataccacgt 1100
54        gtgagagaaa tacatttgga aaacaataaa ctaaaaaaaa tcccttcagg 1150
55        attaccagag ttgaaatacc tccagataat cttccttcat tctaattcaa 1200
56        ttgcaagagt gggagtaaat gacttctgtc caacagtgcc aaagatgaag 1250
57        aaatctttat acagtgcaat aagtttattc aacaacccgg tgaaatactg 1300
58        ggaaatgcaa cctgcaacat ttcgttgtgt tttgagcaga atgagtgttc 1350
59        agcttgggaa ctttggaatg taataattag taattggtaa tgtccattta 1400
60        atataagatt caaaaatccc tacatttgga atacttgaac tctattaata 1450
61        atggtagtat tatatataca agcaaatatc tattctcaag tggtaagtcc 1500
62        actgacttat tttatgacaa gaaatttcaa cggaattttg ccaaactatt 1550
63        gatacataag gggttgagag aaacaagcat ctattgcagt ttcctttttg 1600
64        cgtacaaatg atcttacata aatctcatgc ttgaccattc ctttcttcat 1650
65        aacaaaaaag taagatattc ggtatttaac actttgttat caagcacatt 1700
66        ttaaaaagaa ctgtactgta aatggaatgc ttgacttagc aaaatttgtg 1750
67        ctctttcatt tgctgttaga aaaacagaat taacaaagac agtaatgtga 1800
68        agagtgcatt acactattct tattctttag taacttgggt agtactgtaa 1850
69        tatttttaat catcttaaag tatgatttga tataatctta ttgaaattac 1900
70        cttatcatgt cttagagccc gtctttatgt ttaaaactaa tttcttaaaa 1950
71        taaagccttc agtaaatgtt cattaccaac ttgataaatg ctactcataa 2000
72        gagctggttt ggggctatag catatgcttt ttttttttta attattacct 2050
73        gatttaaaaa tctctgtaaa aacgtgtagt gtttcataaa atctgtaact 2100
74        cgcattttaa tgatccgcta ttataagctt ttaatagcat gaaaattgtt 2150
75        aggctatata acattgccac ttcaactcta aggaatattt ttgagatatc 2200
76        cctttggaag accttgcttg gaagagcctg gacactaaca attctacacc 2250
77        aaattgtctc ttcaaatacg tatggactgg ataactctga gaaacacatc 2300
78        tagtataact gaataagcag agcatcaaat taaacagaca gaaaccgaaa 2350
79        gctctatata aatgctcaga gttctttatg tatttcttat tggcattcaa 2400
80.       catatgtaaa atcagaaaac agggaaattt tcattaaaaa tattggtttg 2450
81        aaat 2454
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84 <211> LENGTH: 379
85 <212> TYPE: PRT
86 <213> ORGANISM: Homo Sapien
87 <400> SEQUENCE: 2
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90        Lys Pro Phe Phe Ser Pro Ser His Ile Ala Leu Lys Asn Met Met
91                         20                  25                  30
92        Leu Lys Asp Met Glu Asp Thr Asp Asp Asp Asp Asp Asp Asp Asp
93                         35                  40                  45
94        Asp Asp Asp Asp Asp Glu Asp Asn Ser Leu Phe Pro Thr Arg Glu
95                         50                  55                  60
96        Pro Arg Ser His Phe Phe Pro Phe Asp Leu Phe Pro Met Cys Pro
97                         65                  70                  75
98        Phe Gly Cys Gln Cys Tyr Ser Arg Val Val His Cys Ser Asp Leu
99                         80                  85                  90
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101                     95                  100                 105
102        Leu Asp Leu Gln Asn Asn Lys Ile Lys Glu Ile Lys Glu Asn Asp
103                    110                  115                 120
104        Phe Lys Gly Leu Thr Ser Leu Tyr Gly Leu Ile Leu Asn Asn Asn
105                    125                  130                 135
106        Lys Leu Thr Lys Ile His Pro Lys Ala Phe Leu Thr Thr Lys Lys
107                    140                  145                 150
108        Leu Arg Arg Leu Tyr Leu Ser His Asn Gln Leu Ser Glu Ile Pro
109                    155                  160                 165
110        Leu Asn Leu Pro Lys Ser Leu Ala Glu Leu Arg Ile His Glu Asn
111                    170                  175                 180
112        Lys Val Lys Lys Ile Gln Lys Asp Thr Phe Lys Gly Met Asn Ala
113                    185                  190                 195
114        Leu His Val Leu Glu Met Ser Ala Asn Pro Leu Asp Asn Asn Gly
115                    200                  205                 210
116        Ile Glu Pro Gly Ala Phe Glu Gly Val Thr Val Phe His Ile Arg
117                    215                  220                 225
118        Ile Ala Glu Ala Lys Leu Thr Ser Val Pro Lys Gly Leu Pro Pro
119                    230                  235                 240
120        Thr Leu Leu Glu Leu His Leu Asp Tyr Asn Lys Ile Ser Thr Val
121                    245                  250                 255
122        Glu Leu Glu Asp Phe Lys Arg Tyr Lys Glu Leu Gln Arg Leu Gly
123                    260                  265                 270
124        Leu Gly Asn Asn Lys Ile Thr Asp Ile Glu Asn Gly Ser Leu Ala
125                    275                  280                 285
126        Asn Ile Pro Arg Val Arg Glu Ile His Leu Glu Asn Asn Lys Leu
127                    290                  295                 300
128        Lys Lys Ile Pro Ser Gly Leu Pro Glu Leu Lys Tyr Leu Gln Ile
129                    305                  310                 315
130        Ile Phe Leu His Ser Asn Ser Ile Ala Arg Val Gly Val Asn Asp
131                    320                  325                 330
132        Phe Cys Pro Thr Val Pro Lys Met Lys Lys Ser Leu Tyr Ser Ala
133                    335                  340                 345
134        Ile Ser Leu Phe Asn Asn Pro Val Lys Tyr Trp Glu Met Gln Pro
135                    350                  355                 360
136        Ala Thr Phe Arg Cys Val Leu Ser Arg Met Ser Val Gln Leu Gly
137                    365                  370                 375
138        Asn Phe Gly Met
140 <210> SEQ ID NO: 3
141 <211> LENGTH: 20
142 <212> TYPE: DNA
143 <213> ORGANISM: Artificial Sequence
144 <220> FEATURE:
145 <223> OTHER INFORMATION: Synthetic Oligonucleotide Probe
146 <400> SEQUENCE: 3
147       ggaaatgagt gcaaaccctc 20
149 <210> SEQ ID NO: 4
150 <211> LENGTH: 24
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151 <212> TYPE: DNA
152 <213> ORGANISM: Artificial Sequence
153 <220> FEATURE:
154 <223> OTHER INFORMATION: Synthetic Oligonucleotide Probe
155 <400> SEQUENCE: 4
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158 <210> SEQ ID NO: 5
159 <211> LENGTH: 50
160 <212> TYPE: DNA
161 <213> ORGANISM: Artificial Sequence
162 <220> FEATURE:
163 <223> OTHER INFORMATION: Synthetic Oligonucleotide Probe
164 <400> SEQUENCE: 5
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167 <210> SEQ ID NO: 6
168 <211> LENGTH: 3441
169 <212> TYPE: DNA
170 <213> ORGANISM: Homo Sapien
171 <400> SEQUENCE: 6
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173         ctccgccctc cgcactcgcg cctccctccc tccgcccgct cccgcgccct 100
174         cctccctccc tcctccccag ctgtcccgtt cgcgtcatgc cgagcctccc 150
175         ggccccgccg gccccgctgc tgctcctcgg gctgctgctg ctcggctccc 200
176         ggccggcccg cggcgccggc ccagagcccc ccgtgctgcc catccgttct 250
177         gagaaggagc cgctgcccgt tcggggagcg gcaggctgca ccttcggcgg 300
178         gaaggtctat gccttggacg agacgtggca cccggaccta gggcagccat 350
179         tcggggtgat gcgctgcgtg ctgtgcgcct gcgaggcgcc tcagtggggt 400
180         cgccgtacca ggggccctgg cagggtcagc tgcaagaaca tcaaaccaga 450
181         gtgcccaacc ccggcctgtg ggcagccgcg ccagctgccg ggacactgct 500
182         gccagacctg cccccaggag cgcagcagtt cggagcggca gccgagcggc 550
183         ctgtccttcg agtatccgcg ggacccggag catcgcagtt atagcgaccg 600
184         cggggagcca ggcgctgagg agcgggcccg tggtgacggc cacacggact 650
185         tcgtggcgct gctgacaggg ccgaggtcgc aggcggtggc acgagcccga 700
186         gtctcgctgc tgcgctctag cctccgcttc tctatctcct acaggcggct 750
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188         ttgagcaccc tgcagccccc acccaagatg gcctggtctg tggggtgtgg 850
189         cgggcagtgc ctcggttgtc tctgcggctc cttagggcag aacagctgca 900
190         tgtggcactt gtgacactca ctcacccttc aggggaggtc tgggggcctc 950
191         tcatccggca ccgggccctg gctgcagaga ccttcagtgc catcctgact 1000
192         ctagaaggcc ccccacagca gggcgtaggg ggcatcaccc tgctcactct 1050
193         cagtgacaca gaggactcct tgcatttttt gctgctcttc cgagggctgc 1100
194         tggaacccag gagtggggga ctaacccagg ttcccttgag gctccagatt 1150
195         ctacaccagg ggcagctact gcgagaactt caggccaatg tctcagccca 1200
196         ggaaccaggc tttgctgagg tgctgcccaa cctgacagtc caggagatgg 1250
197         actggctggt gctggggggag ctgcagatgg ccctggagtg ggcaggcagg 1300
198         ccagggctgc gcatcagtgg acacattgct gccaggaaga gctgcgacgt 1350
199         cctgcaaagt gtcctttgtg gggctgatgc cctgatccca gtccagacgg 1400
200         gtgctgccgg ctcagccagc ctcacgctgc taggaaatgg ctccctgatc 1450
201         tatcaggtgc aagtggtagg gacaagcagt gaggtggtgg ccatgacact 1500
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203        ctggactcca gccaggagga cacacggccg tgggtatctg ccctgggctg 1600
204        ggtgcccgag gggctcatat gctgctgcag aatgagctct tcctgaacgt 1650
205        gggcaccaag gacttcccag acggagagct tcggggggcac gtggctgccc 1700
206        tgccctactg tgggcatagc gcccgccatg acacgctgcc cgtgcccta 1750
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210        cctcctggaa cgccagggcc tcggcggctg ctgaagggat tctatggctc 1950
211        agaggcccag ggtgtggtga aggacctgga gccggaactg ctgcggcacc 2000
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214        actgcgcctg gaggcggccg gggccgaggg ggtgcgggcg ctgggggctc 2150
215        cggatacagc ctctgctgcg ccgcctgtgg tgcctggtct cccggcccta 2200
216        gcgcccgcca aacctggtgg tcctgggcgg ccccgagacc ccaacacatg 2250
217        cttcttcgag gggcagcagc gcccccacgg ggctcgctgg gcgcccaact 2300
218        acgacccgct ctgctcactc tgcacctgcc agagacgaac ggtgatctgt 2350
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231        ccagagacca gaactgatcc agagctggag aaagaagccg aaggctctta 3000
232        gggagcagcc agagggccaa gtgaccaaga ggatggggcc tgagctgggg 3050
233        aaggggtggc atcgaggacc ttcttgcatt ctcctgtggg aagcccagtg 3100
234        cctttgctcc tctgtcctgc ctctactccc accccacta cctctgggaa 3150
235        ccacagctcc acaagggga gaggcagctg ggccagaccg aggtcacagc 3200
236        cactccaagt cctgccctgc caccctcggc ctctgtcctg gaagccccac 3250
237        ccctttcctc ctgtacataa tgtcactggc ttgttgggat ttttaattta 3300
238        tcttcactca gcaccaaggg cccccgacac tccactcctg ctgcccctga 3350
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240        tttcagtcaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaa a 3441
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243 <211> LENGTH: 954
244 <212> TYPE: PRT
245 <213> ORGANISM: Homo Sapien
246 <400> SEQUENCE: 7
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249        Leu Leu Leu Leu Gly Ser Arg Pro Ala Arg Gly Ala Gly Pro Glu
250                        20                 25                  30
251        Pro Pro Val Leu Pro Ile Arg Ser Glu Lys Glu Pro Leu Pro Val
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VERIFICATION SUMMARY
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